ABSTRACT

In one aspect, the invention provides a computer implemented method for transforming a plurality of chromatographic elution profiles, wherein each profile is obtained from the separation of a mixture of homoduplex and heteroduplex molecules by Denaturing Matched Ion Polynucleotide Chromatography. The method preferably includes overlaying the profiles; adjusting the baseline by applying a slope factor to each detector response value so that all of the profiles share a common baseline; normalizing the heights of the peaks to a scale of 1; and shifting the profiles along the x-axis so that all of the profiles intersect at a pre-selected point. In another aspect, the invention provides a method for applying statistical criteria to the transformed profiles to determine whether they represent more that one group. In yet another aspect, the invention concerns methods for grouping the profiles based on their shapes. The methods for applying statistical test and for grouping the profiles include dividing the x-axis into equally spaced regions and determining the distribution of the profiles within the regions. The invention can be used for estimating the number of different single nucleotide polymorphisms in a plurality of test samples and for detecting the presence of a previously unknown polymorphisms. In other aspects, the invention concerns computer systems and computer readable media that can implement and store the data associated with the elution profiles and which can perform the transformation, statistical testing, and grouping processes.